



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/817,530

Source:

IFW0

Date Processed by STIC:

10/5/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFWO

RAW SEQUENCE LISTING

DATE: 10/05/2004

PATENT APPLICATION: US/10/817,530

TIME: 10:34:02

Input Set : A:\Sequence.List.for.10817530.txt

Output Set: N:\CRF4\10052004\J817530.raw

3 <110> APPLICANT: Braun, Werner
 4 Mathura, Venkatarajan S.
 5 Schein, Catherine H.
 7 <120> TITLE OF INVENTION: PHYSICAL-CHEMICAL PROPERTY BASED SEQUENCE MOTIFS AND METHODS
 8 REGARDING SAME
 10 <130> FILE REFERENCE: 265.00400101
 12 <140> CURRENT APPLICATION NUMBER: 10/817,530
 13 <141> CURRENT FILING DATE: 2004-04-02
 15 <150> PRIOR APPLICATION NUMBER: US 60/460,769
 16 <151> PRIOR FILING DATE: 2003-04-04
 18 <160> NUMBER OF SEQ ID NOS: 5
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 10
 24 <212> TYPE: PRT
 C--> 25 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
 W--> 27 <220> FEATURE:
 W--> 27 <223> OTHER INFORMATION: *delete; give source of genetic material*
 W--> 27 <400> 1
 29 Pro Asp Ile Leu Cys Leu Gln Glu Thr Lys
 30 1 5 10
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 275
 35 <212> TYPE: PRT
 C--> 36 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
 W--> 38 <220> FEATURE:
 W--> 38 <223> OTHER INFORMATION: *move down to <223> line*
 W--> 38 <400> 2
 40 Leu Tyr Glu Asp Pro Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro
 41 1 5 10 15
 44 Ala Thr Leu Lys Ile Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp
 45 20 25 30
 48 Ile Lys Lys Lys Gly Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile
 49 35 40 45
 52 Leu Cys Leu Gln Glu Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu
 53 50 55 60
 56 Leu Gln Glu Leu Pro Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser
 57 65 70 75 80
 60 Asp Lys Glu Gly Tyr Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro
 61 85 90 95
 64 Leu Lys Val Ser Tyr Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly
 65 100 105 110
 68 Arg Val Ile Val Ala Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr

pp 1-4, 6
Does Not Comply
Corrected Diskette Needed

Per 1.823 of Sequence Rules, the explanation for Artificial Sequence goes on <223> line. Please insert a <220> above <223>. Do not insert response to <220> - it is a header only. see p. 6 for error explanation.

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Input Set : A:\Sequence.List.for.10817530.txt

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```

69          115          120          125
72 Val Pro Asn Ala Gly Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg
73          130          135          140
76 Trp Asp Glu Ala Phe Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys
77 145          150          155          160
80 Pro Leu Val Leu Cys Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp
81          165          170          175
84 Leu Arg Asn Pro Lys Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln
85          180          185          190
88 Glu Arg Gln Gly Phe Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp
89          195          200          205
92 Ser Phe Arg His Leu Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp
93          210          215          220
96 Thr Tyr Met Met Asn Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp
97 225          230          235          240
100 Tyr Phe Leu Leu Ser His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys
101          245          250          255
104 Ile Arg Ser Lys Ala Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr
105          260          265          270
108 Leu Ala Leu
109          275
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 268
114 <212> TYPE: PRT
C--> 115 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
W--> 117 <220> FEATURE:
W--> 117 <223> OTHER INFORMATION:
W--> 117 <400> 3
119 Met Lys Phe Val Ser Phe Asn Ile Asn Gly Leu Arg Ala Arg Pro His
120 1          5          10          15
123 Gln Leu Glu Ala Ile Val Glu Lys His Gln Pro Asp Val Ile Gly Leu
124          20          25          30
127 Gln Glu Thr Lys Val His Asp Asp Met Phe Pro Leu Glu Glu Val Ala
128          35          40          45
131 Lys Leu Gly Tyr Asn Val Phe Tyr His Gly Gln Lys Gly His Tyr Gly
132          50          55          60
135 Val Ala Leu Leu Thr Lys Glu Thr Pro Ile Ala Val Arg Arg Gly Phe
136 65          70          75          80
139 Pro Gly Asp Asp Glu Glu Ala Gln Arg Arg Ile Ile Met Ala Glu Ile
140          85          90          95
143 Pro Ser Leu Leu Gly Asn Val Thr Val Ile Asn Gly Tyr Phe Pro Gln
144          100          105          110
147 Gly Glu Ser Arg Asp His Pro Ile Lys Phe Pro Ala Lys Ala Gln Phe
148          115          120          125
151 Tyr Gln Asn Leu Gln Asn Tyr Leu Glu Thr Glu Leu Lys Arg Asp Asn
152          130          135          140
155 Pro Val Leu Ile Met Gly Asp Met Asn Ile Ser Pro Thr Asp Leu Asp
156 145          150          155          160
159 Ile Gly Ile Gly Glu Glu Asn Arg Lys Arg Trp Leu Arg Thr Gly Lys

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```

160                               165                               170                               175
163 Cys Ser Phe Leu Pro Glu Glu Arg Glu Trp Met Asp Arg Leu Met Ser
164                               180                               185                               190
167 Trp Gly Leu Val Asp Thr Phe Arg His Ala Asn Pro Gln Thr Ala Asp
168                               195                               200                               205
171 Arg Phe Ser Trp Phe Asp Tyr Arg Ser Lys Gly Phe Asp Asp Asn Arg
172                               210                               215                               220
175 Gly Leu Arg Ile Asp Leu Leu Leu Ala Ser Gln Pro Leu Ala Glu Cys
176 225                               230                               235                               240
179 Cys Val Glu Thr Gly Ile Asp Tyr Glu Ile Arg Ser Met Glu Lys Pro
180                               245                               250                               255
183 Ser Asp His Ala Pro Val Trp Ala Thr Phe Arg Arg
184                               260                               265
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 258
189 <212> TYPE: PRT
-> 190 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
-> 192 <220> FEATURE:
-> 192 <223> OTHER INFORMATION:
-> 192 <400> 4
194 Leu Lys Ile Ala Ala Phe Asn Ile Arg Thr Phe Gly Glu Thr Lys Met
195 1                               5                               10                               15
198 Ser Asn Ala Thr Leu Ala Ser Tyr Ile Val Arg Ile Val Arg Arg Tyr
199                               20                               25                               30
202 Asp Ile Val Leu Ile Gln Glu Val Arg Asp Ser His Leu Val Ala Val
203                               35                               40                               45
206 Gly Lys Leu Leu Asp Tyr Leu Asn Gln Asp Asp Pro Asn Thr Tyr His
207                               50                               55                               60
210 Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
211 65                               70                               75                               80
214 Leu Phe Leu Phe Arg Pro Asn Lys Val Ser Val Leu Asp Thr Tyr Gln
215                               85                               90                               95
218 Tyr Asp Asp Gly Cys Cys Gly Asn Asp Ser Phe Ser Arg Glu Pro Ala
219                               100                               105                               110
222 Val Val Lys Phe Ser Ser His Ser Thr Lys Val Lys Glu Phe Ala Ile
223                               115                               120                               125
226 Val Ala Leu His Ser Ala Pro Ser Asp Ala Val Ala Glu Ile Asn Ser
227                               130                               135                               140
230 Leu Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
231 145                               150                               155                               160
234 Val Met Leu Met Gly Asp Phe Asn Ala Asp Cys Ser Tyr Val Thr Ser
235                               165                               170                               175
238 Ser Gln Trp Ser Ser Ile Arg Leu Arg Thr Ser Ser Thr Phe Gln Trp
239                               180                               185                               190
242 Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Ser Thr Asn Cys Ala
243                               195                               200                               205
246 Tyr Asp Arg Ile Val Val Ala Gly Ser Leu Leu Gln Ser Ser Val Val
247                               210                               215                               220
250 Pro Gly Ser Ala Ala Pro Phe Asp Phe Gln Ala Ala Tyr Gly Leu Ser

```

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```

251 225                230                235                240
254 Asn Glu Met Ala Leu Ala Ile Ser Asp His Tyr Pro Val Glu Val Thr
255                245                250                255
258 Leu Thr

```

262 <210> SEQ ID NO: 5

263 <211> LENGTH: 336

264 <212> TYPE: PRT

C--> 265 <213> ORGANISM: ARTIFICIAL; MEMBER OF DNase-I SUPERFAMILY

W--> 267 <220> FEATURE:

W--> 267 <223> OTHER INFORMATION:

W--> 267 <400> 5

269 Tyr Asp Pro Ile His Glu Tyr Val Asn His Glu Leu Arg Lys Arg Glu
270 1 5 10 15

273 Asn Glu Phe Ser Glu His Lys Asn Val Lys Ile Phe Val Ala Ser Tyr
274 20 25 30

277 Asn Leu Asn Gly Cys Ser Ala Thr Thr Lys Leu Glu Asn Trp Leu Phe
278 35 40 45

281 Pro Glu Asn Thr Pro Leu Ala Asp Ile Tyr Val Val Gly Phe Gln Glu
282 50 55 60

285 Ile Val Gln Leu Thr Ser Ala Asp Pro Ala Lys Arg Arg Glu Trp Glu
286 65 70 75 80

289 Ser Cys Val Lys Arg Leu Leu Asn Gly Lys Cys Thr Ser Gly Pro Gly
290 85 90 95

293 Tyr Val Gln Leu Arg Ser Gly Gln Leu Val Gly Thr Ala Leu Met Ile
294 100 105 110

297 Phe Cys Lys Glu Ser Cys Leu Pro Ser Ile Lys Asn Val Glu Gly Thr
298 115 120 125

301 Val Lys Lys Thr Gly Leu Gly Asn Lys Gly Ala Val Ala Ile Arg Phe
302 130 135 140

305 Asp Tyr Glu Asp Thr Gly Leu Cys Phe Ile Thr Ser His Leu Ala Ala
306 145 150 155 160

309 Gly Tyr Thr Asn Tyr Asp Glu Arg Asp His Asp Tyr Arg Thr Ile Ala
310 165 170 175

313 Ser Gly Leu Arg Phe Arg Arg Gly Arg Ser Ile Phe Asn His Asp Tyr
314 180 185 190

317 Val Val Trp Phe Gly Asp Phe Asn Tyr Arg Ile Ser Leu Thr Tyr Glu
318 195 200 205

321 Glu Val Val Pro Cys Ile Ala Gln Gly Lys Leu Ser Tyr Leu Phe Glu
322 210 215 220

325 Tyr Asp Gln Leu Asn Lys Gln Met Leu Thr Gly Lys Val Phe Pro Phe
326 225 230 235 240

329 Phe Ser Glu Leu Pro Ile Thr Phe Pro Pro Thr Tyr Lys Phe Asp Ile
330 245 250 255

333 Gly Thr Asp Ile Tyr Asp Thr Ser Asp Lys His Arg Val Pro Ala Trp
334 260 265 270

337 Thr Asp Arg Ile Leu Tyr Arg Gly Glu Leu Val Pro His Ser Tyr Gln

341 Ser Val Pro Leu Tyr Tyr Ser Asp His Arg Pro Ile Tyr Ala Thr Tyr

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Input Set : A:\Sequence.List.for.10817530.txt

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345	Glu	Ala	Asn	Ile	Val	Lys	Val	Asp	Arg	Glu	Lys	Lys	Lys	Ile	Leu	Phe
346	305				310					315					320	
349	Glu	Glu	Leu	Tyr	Asn	Gln	Arg	Lys	Gln	Glu	Val	Arg	Asp	Ala	Ser	Gln
350					325					330					335	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/817,530

DATE: 10/05/2004
TIME: 10:34:03

Input Set : A:\Sequence.List.for.10817530.txt
Output Set: N:\CRF4\10052004\J817530.raw

error explanation

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5

VERIFICATION SUMMARY

DATE: 10/05/2004

PATENT APPLICATION: US/10/817,530

TIME: 10:34:03

Input Set : A:\Sequence.List.for.10817530.txt

Output Set: N:\CRF4\10052004\J817530.raw

L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:27 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:27 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:36 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:38 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:38 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:38
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:117 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:117 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:117 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:117
L:190 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:192
L:265 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:267 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:267 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:267